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## SEQUENCE LISTING

<110> Bureau of Sugar Experiment Stations
 The University of Queensland

<120> A bioreactor system

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<160> 53

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Le	ı Ala	a Th:		e Ly:	s Sei	туз	Ala 280	Asr )	n Ala	a Gly	y Val	. Asr 285	Pro	o FA:	s Val

420

480

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- Trp Asp Ser Thr Lys Thr Ala Phe Asp Lys Val Lys Ser Glu Val Gly 65 70 75 80
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- Leu Thr Ser Leu Phe Asn Val Thr Lys Gln Val Ile Asp Gly Met Ala
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- Lys Gly Gln Phe Gly Gln Thr Asn Tyr Ser Thr Ala Lys Ala Gly Leu 145 150 155 160
- His Gly Phe Thr Met Ala Leu Ala Gln Glu Val Ala Thr Lys Gly Val 165 170 175
- Thr Val Asn Thr Val Ser Pro Gly Tyr Ile Ala Thr Asp Met Val Lys

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Lys Arg Leu Gly Leu Pro Glu Glu Ile Ala Ser Ile Cys Ala Trp Leu 210 215 220

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					acc Thr											624
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Pro Ala Gln Leu Gly Asp Ile Gln Gln Arg Tyr Met Lys Asp Phe Ser

Ala Leu Trp Gln Ala Met Ala Glu Gly Lys Ala Glu Ala Thr Gly Pro • 90

Leu His Asp Arg Arg Phe Ala Gly Asp Ala Trp Arg Thr Asn Leu Pro

Tyr Arg Phe Ala Ala Ala Phe Tyr Leu Leu Asn Ala Arg Ala Leu Thr

Glu Leu Ala Asp Ala Val Glu\ Ala Asp Ala Lys Thr Arg Gln Arg Ile 135

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Pro Gly Pro Trp Tyr Cys Trp Tyr Leu Arg His Thr Tyr Leu Gln Asn 435 440 445

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Asn Lys Leu Arg Phe Val Leu Gly Ala Ser Gly His Ile Ala Gly Val 500 505 510

Ile Asn Pro Pro Ala Lys Asn Lys Arg Ser His Trp Thr Asn Asp Ala 515 520 525

Leu Pro Glu Ser Pro Gln Gln Trp Leu Ala Gly Ala Ile Glu His His 530 535 540

Gly Ser Trp Trp Pro Asp Trp Thr Ala Trp Leu Ala Gly Gln Ala Gly 545 550 560

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Ser Arg Gly Gln Ser Ala Ala Met Ala Pro Phe Gly Gly Leu Lys Ser 20 25 30	
atg act gga ttc cca gtg aag aag gtc aac act gac att act tcc att	144
Met Thr Gly Phe Pro Val Lys Lys Val Asn Thr Asp Ile Thr Ser Ile 35 40 45	
aca age aat ggt gga aga gta aag tge atg cag gtg tgg cet cea att	192
Thr Ser Asn Gly Gly Arg Val Lys Cys Met Gln Val Trp Pro Pro Ile 50 60	
gga aag aag ttt gag act ctt tcc tat ttg cca cca ttg acc aga	240
Gly Lys Lys Phe Glu Thr Leu Ser Tyr Leu Pro Pro Leu Thr Arg 65 70 75 80	
gat tee egg gtg act gae gtt gte ate gta tee gee gee ege ace geg	288
Asp Ser Arg Val Thr Asp Val Val Ile Val Ser Ala Ala Arg Thr Ala 85 90 95	
gtc ggc aag ttt ggc ggc tcg ctg gcc aag atc ccg gca ccg gaa ctg	336
Val Gly Lys Phe Gly Gly Ser Leu Ala Lys Ile Pro Ala Pro Glu Leu 100 105 110	
ggt gcc gtg gtc atc aag gcc gcg ctg gag cgc gcc ggc gtc aag ccg	384
Gly Ala Val Val Ile Lys Ala Ala Leu Glu Arg Ala Gly Val Lys Pro 115 120 125	
gag cag gtg agc gaa gtc atc atg ggc cag gtg ctg acc gcc ggt tcg	432
Glu Gln Val Ser Glu Val Ile Met Gly Gln Val Leu Thr Ala Gly Ser	<b>S</b>

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ggc Gly 145										gcg Ala 160	. 480
atg Met											528
gcc Ala											576
gtg Val							Ala				624
ccg Pro											672
acc Thr 225	-	_	_	 _	 _			_		_	720
ggc Gly											768
gcg Ala								Āla			816
cag Gln	Lys										864
cag Gln											912
cag Gln 305											960
aag Lys											1008
gcc Ala											1056
ctg Leu											1104

50

ccc Pro	aag Lys 370	gtg Val	atg Met	ggc Gly	atg Met	ggc Gly 375	ccg Pro	gtg Val	ccg Pro	gcc Ala	tcc Ser 380	aag Lys	cgc Arg	gcc Ala	ctg Leu	1152
tcg Ser 385	cgc Arg	gcc Ala	gag Glu	tgg Trp	acc Thr 390	ccg Pro	caa Gln	gac Asp	ctg Leu	gac Asp 395	ctg Leu	atg Met	gag Glu	atc Ile	aac Asn 400	1200
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gac Asp	acc Thr	tcc Ser	aag Lys 420	gtc Val	aat Asn	gtg Val	aac Asn	ggc Gly 425	ggc Gly	gcc Ala	atc Ile	gcc Ala	atc Ile 430	ggc Gly	cac His	1296
ccg Pro	atc Ile	ggc Gly 435	gcg Ala	tcg Ser	ggc Gly	tgc Cys	cgt Arg 440	atc Ile	ctg Leu	gtg Val	acg Thr	ctg Leu 445	ctg Leu	cac His	gag Glu	1344
atg Met	aag Lys 450	cgc Arg	cgt Arg	gac Asp	gcg Ala	aag Lys 455	aag Lys	ggc Gly	ctg Leu	gcc Ala	tcg Ser 460	ctg Leu	tgc Cys	atc Ile	ggc	1392
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Ser	Arg	gly	Gln 20	Ser	Ala	Ala	Met	Ala 25	Pro	Phe	e Gly	Gly	Leu 30	Lys	Ser	
Met	Thr	Gl <sub>y</sub> 35	y Phe	Pro	Val	. Lys	Lys 40	val	. Asr	Thr	: Asp	11e 45	. Thr	Ser	: Ile	

Thr Ser Asn Gly Gly Arg Val Lys Cys Met Gln Val Trp Pro Pro Ile 50 60 .

- Gly Lys Lys Lys Phe Glu Thr Leu Ser Tyr Leu Pro Pro Leu Thr Arg 65 70 75 80
- Asp Ser Arg Val Thr Asp Val Val Ile Val Ser Ala Ala Arg Thr Ala 85 . 90 95
- Val Gly Lys Phe Gly Gly Ser Leu Ala Lys Ile Pro Ala Pro Glu Leu 100 105 110
- Gly Ala Val Val Ile Lys Ala Ala Leu Glu Arg Ala Gly Val Lys Pro 115 120 125
- Glu Gln Val Ser Glu Val Ile Met Gly Gln Val Leu Thr Ala Gly Ser 130 135 140
- Gly Gln Asn Pro Ala Arg Gln Ala Ala Ile Lys Ala Gly Leu Pro Ala 145 150 . 155 160
- Met Val Pro Ala Met Thr Ile Asn Lys Val Cys Gly Ser Gly Leu Lys 165 170 175
- Ala Val Met Leu Ala Ala Asn Ala Ile Met Ala Gly Asp Ala Glu Ile 180 185 190
- Val Val Ala Gly Gly Gln Glu Asn Met Ser Ala Ala Pro His Val Leu 195 200 205
- Pro-Gip-Wer Arg Asp Gly Phe Arg Met Gly Asp Ala Lys Leu Val Asp 210 215 220
- Thr Met Ile Val Asp Gly Leu Trp Asp Val Tyr Asn Gln Tyr His Met 225 230 235 240
- Gly Ile Thr Ala Glu Asn Val Ala Lys Glu Tyr Gly Ile Thr Arg Glu 245 250 255
- Ala Gln Asp Glu Phe Ala Val Gly Ser Gln Asn Lys Ala Glu Ala Ala 260 265 270
- Gln Lys Ala Gly Lys Phe Asp Glu Glu Ile Val Pro Val Leu Ile Pro 275 280 285

Gln Arg Lys Gly Asp Pro Val Ala Phe Lys Thr Asp Glu Phe Val Arg 290 295 300

Gln Gly Ala Thr Leu Asp Ser Met Ser Gly Leu Lys Pro Ala Phe Asp 305 310 315 320

Lys Ala Gly Thr Val Thr Ala Ala Asn Ala Ser Gly Leu Asn Asp Gly 325 330 335

Ala Ala Val Val Wet Ser Ala Ala Lys Ala Lys Glu Leu Gly 340 345 350

Leu Thr Pro Leu Ala Thr Ile Lys Ser Tyr Ala Asn Ala Gly Val Asp 355 . 360 365

Pro Lys Val Met Gly Met Gly Pro Val Pro Ala Ser Lys Arg Ala Leu 370 375 380

Ser Arg Ala Glu Trp Thr Pro Gln Asp Leu Asp Leu Met Glu Ile Asn 385 390 395 400

Glu Ala Phe Ala Ala Gln Ala Leu Ala Val His Gln Gln Met Gly Trp 405 410 415

Asp Thr Ser Lys Val Asn Val Asn Gly Gly Ala Ile Ala Ile Gly His
420 425 430

Pro Ile Gly Ala Ser Gly Cys Arg Ile Leu Val Thr Leu Leu His Glu

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<211> 1529

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<213> Rastonia Eutropia

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tgcaggtgtg	gcctccaatt	ggaaagaaga	agtttgagac	tctttcctat	ttgccaccat	240
tgaccagaga	ttcccgggtg	actgacgttg	tcatcgtatc	cgccgcccgc	accgcggtcg	300
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ccdc <del>ddadd</del> e	ggtgatgtcg	gcggccaagg	ccaaggaact	gggcctgacc	ccgctggcca	1080
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145				150					155					160	
gag gt Glu Va	tc gg al Gl	c gag y Glu	gtt Val 165	gat Asp	gtg Val	ctg Leu	atc Ile	aac Asn 170	aac Asn	gcc Ala	ggt Gly	atc Ile	acc Thr 175	cgc Arg	528
gac gt Asp Va	tg gt al Va	g ttc 1 Phe 180	cgc Arg	aag Lys	atg Met	acc Thr	cgc Arg 185	gcc Ala	gac Asp	tgg Trp	gat Asp	gcg Ala 190	gtg Val	atc Ile	576
gac ac Asp Ti	cc aa hr As 19	n Leu	acc Thr	tcg Ser	ctg Leu	ttc Phe 200	aac Asn	gtc Val	acc Thr	aag Lys	cag Gln 205	gtg Val	atc Ile	gac Asp	624
ggc at Gly Me 2:	tg gc et Al 10	c gac a Asp	cgt Arg	ggc Gly	tgg Trp 215	ggc Gly	cgc Arg	atc Ile	gtc Val	aac Asn 220	atc Ile	tcg Ser	tcg Ser	gtg Val	672
aac g Asn G 225	gg ca ly Gl	g aag n Lys	ggc Gly	cag Gln 230	ttc Phe	ggc	cag Gln	acc Thr	aac Asn 235	tac Tyr	tcc Ser	acc Thr	gcc Ala	aag Lys 240	720
gcc g Ala G	gc ct ly Le	g cat u His	ggc Gly 245	ttc Phe	acc Thr	atg Met	gca Ala	ctg Leu 250	gcg Ala	cag Gln	gaa Glu	gtg Val	gcg Ala 255	acc Thr	768
aag g Lys G	gc gt ly Va	g acc l Thr 260	Val	aac Asn	acg Thr	gtc Val	tct Ser 265	ccg Pro	ggc	tat Tyr	atc Ile	gcc Ala 270	acc Thr	gac Asp	816
atg g Met V	rtc aa Val Ly 27	s Ala	atc Ile	cgc Arg	cag Gln	gac Asp 280	gtg Val	ctc Leu	gac Asp	aag Lys	atc Ile 285	gtc Val	gcg Ala	acg Thr	864
Ile P	ccg gt Pro Va 290	c aag al Lys	cgc Arg	ctg Leu	ggc Gly 295	ctg Leu	cca Pro	gaa Glu	gag Glu	atc Ile 300	gcc Ala	tcg Ser	atc Ile	tgc Cys	912
gcc t Ala T 305	gg tt Trp Le	g tog eu Ser	tcg Ser	gag Glu 310	gag Glu	tcc Ser	ggt Gly	ttc Phe	tcg Ser 315	Thr	ggc	gcc Ala	gac Asp	ttc Phe 320	960
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<211> 329

<212> PRT

<213> Rastonia Eutropia

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Met Thr Gly Phe Pro Val Lys Lys Val Asn Thr Asp Ile Thr Ser Ile 35 40 45

Thr Ser Asn Gly Gly Arg Val Lys Cys Met Gln Val Trp Pro Pro Ile 50 55 60

Gly Lys Lys Lys Phe Glu Thr Leu Ser Tyr Leu Pro Pro Leu Thr Arg 65 70 75 80

Asp Ser Arg Val Thr Gln Arg Ile Ala Tyr Val Thr Gly Gly Met Gly 85 90 95

Gly Ile Gly Thr Ala Ile Cys Gln Arg Leu Ala Lys Asp Gly Phe Arg 100 105 110

Val Val Ala Gly Cys Gly Pro Asn Ser Pro Arg Arg Glu Lys Trp Leu 115 120 125

Glu Gln Gln Lys Ala Leu Gly Phe Asp Phe Ile Ala Ser Glu Gly Asn 130 135 140

Val Ala Asp Trp Asp Ser Thr Lys Thr Ala Phe Asp Lys Val Lys Ser 145 150 155 160

Glu Val Gly Glu Val Asp Val Leu Ile Asn Asn Ala Gly Ile Thr Arg 165 170 175

Asp Val Val Phe Arg Lys Met Thr Arg Ala Asp Trp Asp Ala Val Ile 180 185 190

Asp Thr Asn Leu Thr Ser Leu Phe Asn Val Thr Lys Gln Val Ile Asp 195 200 205

Gly Met Ala Asp Arg Gly Trp Gly Arg Ile Val Asn Ile Ser Ser Val 210 215 220 Asn Gly Gln Lys Gly Gln Phe Gly Gln Thr Asn Tyr Ser Thr Ala Lys 225 230

Ala Gly Leu His Gly Phe Thr Met Ala Leu Ala Gln Glu Val Ala Thr 250 245

Lys Gly Val Thr Val Asn Thr Val Ser Pro Gly Tyr Ile Ala Thr Asp 265 260

Met Val Lys Ala Ile Arg Gln Asp Val Leu Asp Lys Ile Val Ala Thr 280 275

Ile Pro Val Lys Arg Leu Gly Leu Pro Glu Glu Ile Ala Ser Ile Cys 295 290

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<213> Rastonia Eutropia

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	<b>.</b>		+-				ataa	· ~~+	. ~ ~ ~ ~	+~-	+000	C2CC		ratas	cctc	g 600
gtgt																
ctgt	tcaa	.cg t	caco	aago	a gg	gtgat	cgac	ggc	atgg	ccg	accg	tggc	tg q	gggco	gcat	c 660
gtca	acat	ct c	gtcg	gtga	a co	ggca	ıgaag	ggc	cagt	tcg	gcca	gaco	aa c	ctact	ccac	c 720
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tct Ser																96
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aca Thr																192
gga Gly	aag Lys	aag Lys	aag Lys	ttt Phe	gag Glu	act Thr	ctt Leu	tcc Ser	tat Tyr	ttg Leu	cca Pro	cca Pro	ttg Leu	acc Thr	aga Arg	240

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65	70	75	80
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ggc aag tcc caa cca Gly Lys Ser Gln Pro 100	ttc aag gtc acg cc Phe Lys Val Thr Pro 105	g ggg cca ttc gat cc o Gly Pro Phe Asp Pro 110	a gcc 336 o Ala
		g ggc act gaa ggc aa n Gly Thr Glu Gly As: 125	
cac gcg gcc gcg tcc His Ala Ala Ala Ser 130	ggc att ccg ggc ctc Gly Ile Pro Gly Le 135	g gat gcg ctg gca gg u Asp Ala Leu Ala Gl 140	c gtc 432 y Val
aag atc gcg ccg gcg Lys Ile Ala Pro Ala 145	cag ctg ggt gat at Gln Leu Gly Asp Ilo 150	c cag cag cgc tac at e Gln Gln Arg Tyr Me 155	g aag 480 t Lys 160
gac ttc tca gcg ctg Asp Phe Ser Ala Leu 165	tgg cag gcc atg gc Trp Gln Ala Met Ala 17	c gag ggc aag gcc ga a Glu Gly Lys Ala Gl 0 17	u Ala
		c ggc gac gca tgg cg a Gly Asp Ala Trp Ar 190	
		c tac ctg ctc aat gc e Tyr Leu Leu Asn Al 205	
		g gcc gat gcc aag ac u Ala Asp Ala Lys Th 220	
		g gtc gat gcg atg tc p Val Asp Ala Met Se 235	
	Thr Asn Pro Glu Al	g cag cgc ctg ctg at a Gln Arg Leu Leu Il 0 25	e Glu
		g cgc aac atg atg ga l Arg Asn Met Met Gl 270	
		c gag agc gcg ttt ga p Glu Ser Ala Phe Gl 285	
		c gtg gtc ttc gag aa a Val Val Phe Glu As 300	

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cgc Arg	ccg Pro	ctg Leu	ctg Leu	atg Met 325	gtg Val	ccg Pro	ccg Pro	tgc Cys	atc Ile 330	aac Asn	aag Lys	tac Tyr	tac Tyr	atc Ile 335	ctg Leu	1008
gac Asp	ctg Leu	cag Gln	ccg Pro 340	gag Glu	agc Ser	tcg Ser	ctg Leu	gtg Val 345	cgc Arg	cat His	gtg Val	gtg Val	gag Glu 350	cag Gln	gga Gly	1056
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Gly Lys Lys Lys Phe Glu Thr Leu Ser Tyr Leu Pro Pro Leu Thr Arg
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Gly Lys Ser Gln Pro Phe Lys Val Thr Pro Gly Pro Phe Asp Pro Ala 100 105 110

Thr Trp Leu Glu Trp Ser Arg Gln Trp Gln Gly Thr Glu Gly Asn Gly 115 120 125

His Ala Ala Ala Ser Gly Ile Pro Gly Leu Asp Ala Leu Ala Gly Val 130 135 140

Lys Ile Ala Pro Ala Gln Leu Gly Asp Ile Gln Gln Arg Tyr Met Lys 145 150 155 160

Asp Phe Ser Ala Leu Trp Gln Ala Met Ala Glu Gly Lys Ala Glu Ala 165 170 175

Thr Gly Pro Leu His Asp Arg Arg Phe Ala Gly Asp Ala Trp Arg Thr .
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Ala Leu Thr Glu Leu Ala Asp Ala Val Glu Ala Asp Ala Lys Thr Arg 210 215 220

Gln Arg Ile Arg Phe Ala Ile Ser Gln Trp Val Asp Ala Met Ser Pro 225 230 235 240

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Ser Gly Glu Ser Leu Arg Ala Gly Val Arg Asn Met Met Glu Asp

- 32 -

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Gly	Arg 290	Asn	Val	Ala	Val	Thr 295	Glu	Gly	Ala	Val	Val 300	Phe	Glu	Asn	Glu
Tyr 305	Phe	Gln	Leu	Leu	Gln 310	Tyr	Lys	Pro	Leu	Thr 315	Asp	Lys	Val	His	Ala 320
Arg	Pro	Leu	Leu	Met 325	Val	Pro	Pro	Cys	Ile 330	Asn	Lys	Tyr	Tyr	Ile 335	Let
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His	Thr	Val 355	Phe	Leu	Val	Ser	Trp 360	Arg	Asn	Pro	Asp	Ala 365	Ser	Met	Ala
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His	Val 450	Gln	Leu	Arg	Glu	Ala 455	Thr	Leu	Gly	Gly	Gly 460	Ala	Gly	Ala	Pro
Cys 465	Ala	Leu	Leu	Arg	Gly 470	Leu	Glu	Leu	Ala	Asn 475	Thr	Phe	Ser	Phe	Let 480
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•

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Thr Asn Leu Pro Gly Pro Trp Tyr Cys Trp Tyr Leu Arg His Thr Tyr 515 520 525

Leu Gln Asn Glu Leu Lys Val Pro Gly Lys Leu Thr Val Cys Gly Val 530 535 540

Pro Val Asp Leu Ala Ser Ile Asp Val Pro Thr Tyr Ile Tyr Gly Ser 545 550 555 560

Arg Glu Asp His Ile Val Pro Trp Thr Ala Ala Tyr Ala Ser Thr Ala 565 570 575

Leu Leu Ala Asn Lys Leu Arg Phe Val Leu Gly Ala Ser Gly His Ile 580 585 590

Ala Gly Val Ile Asn Pro Pro Ala Lys Asn Lys Arg Ser His Trp Thr 595 600 605

Asn Asp Ala Leu Pro Glu Ser Pro Gln Gln Trp Leu Ala Gly Ala Ile 610 615 620

Glu His His Gly Ser Trp Trp Pro Asp Trp Thr Ala Trp Leu Ala Gly 625 630 635 640

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115

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Lys Arg Phe Phe Glu Thr Gly Gly Lys Ser Leu Leu Asp Gly Leu Gly 150

His Leu Ala Lys Asp Leu Val Asn Asn Gly Gly Met Pro Ser Gln Val 170 165

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Gln	Ser	Ile	Leu	Asn 485	Pro	Pro	Gly	Asn	Pro 490	Lys	Ala	Arg	Phe	Met 495	Thr
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Arg	Ser 530		Lys	Thr	Arg	Lys 535		Pro	Ala	Ser	Leu 540	Gly	Asn	Lys	Thr
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Tyr Leu Ala Trp Arg Lys Glu Leu His Ser Trp Ile Ser His Ser Asp 100 105 110	
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115 120 125	
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											aag Lys					960
											aat Asn					1008
											aag Lys					1056
											aag Lys					1104
											gtc Val 380					1152
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tat Tyr 545	Pro	gco Ala	ggc Gly	gaa Glu	gcc Ala 550	Ala	ccc Pro	gga Gly	acc Thr	tac Tyr 555	· val	g cat L His	gaa Glu	a cga	s tca Ser 560	1680
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acç Thi	g ago	g ccq	g gga 580	Ala	gct Ala	gga a Gly	a ato	g ggc t Gly 589	y GI:	a ggg ı Gly	g act	t ago r Sei	c cti r Lei 590	ı va	g gtg l Val	1776
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Ser Ala Arg His Val Ala His Phe Ser Leu Glu Leu Lys Asn Val Leu

Leu Gly Gln Ser Glu Leu Arg Pro Gly Asp Asp Asp Arg Arg Phe Ser

Asp Pro Ala Trp Ser Gln Asn Pro Leu Tyr Lys Arg Tyr Met Gln Thr

Tyr Leu Ala Trp Arg Lys Glu Leu His Ser Trp Ile Ser His Ser Asp . . . 100 105

Leu Ser Pro Gln Asp Ile Ser Arg Gly Gln Phe Val Ile Asn Leu Leu 120 115

Thr Glu Ala Met Ser Pro Thr Asn Ser Leu Ser Asn Pro Ala Ala Val 135 130

Lys Arg Phe Phe Glu Thr Gly Gly Lys Ser Leu Leu Asp Gly Leu Gly 150 155 145

His Leu Ala Lys Asp Leu Val Asn Asn Gly Gly Met Pro Ser Gln Val 170 165

Asp Met Asp Ala Phe Glu Val Gly Lys Asn Leu Ala Thr Thr Glu Gly

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Thr	Gln	Leu	Val	Ser 325	Val	Leu	Asp	Phe	Glu 330	Leu	Asn	Thr	Gln	Val 335	Ala
Leu	Phe	Ala	Asp 340	Glu	Lys	Thr	Leu	Glu 345	Ala	Ala	Lys	Arg	Arg 350	Ser	Tyr
Gln	Ser	Gly 355	Val	Leu	Glu	Gly	Lys 360	Asp	Met	Ala	Lys	Val 365	Phe	Ala	Trp
Met	Arg 370	Pro	Asn	Asp	Leu	Ile 375	Trp	Asn	Tyr	Trp	Val 380	Asn	Asn	Tyr	Leu
Leu 385	Gly	Asn	Gln	Pro	Pro 390	Ala	Phe	Asp -	Ile	Leu 395	Tyr	Trp	Asn ·	Asn	Asp 400
Thr	Thr	Arg	Leu	Pro 405	Ala	Ala	Leu		Gly 410	Glu	Phe	Val	Glu	Leu 415	Phe

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Pro Ile Asp Leu Lys Gln Val Thr Cys Asp Phe Tyr Cys Val Ala Gly 435 440 445

Leu Asn Asp His Ile Thr Pro Trp Glu Ser Cys Tyr Lys Ser Ala Arg 450 455 460

Leu Leu Gly Gly Lys Cys Glu Phe Ile Leu Ser Asn Ser Gly His Ile 465 470 475 480

Gln Ser Ile Leu Asn Pro Pro Gly Asn Pro Lys Ala Arg Phe Met Thr 485 490 495

Asn Pro Glu Leu Pro Ala Glu Pro Lys Ala Trp Leu Glu Gln Ala Gly 500 505 510

Lys His Ala Asp Ser Trp Trp Leu His Trp Gln Gln Trp Leu Ala Glu 515 520 525

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Tyr Pro Ala Gly Glu Ala Ala Pro Gly Thr Tyr Val His Glu Arg Ser 545 550 555

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nec i		35	riie	110	Val	БуЗ	40	Vai	non	1111	voħ	45	1111	Ser	116	
aca a																192
Thr S	ser 50	Asn	СТĀ	стА	Arg	55	гÀг	Cys	met	GIN	Val	Trp	Pro	Pro	He	
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Asp S	Ser	Arg	Vaĺ	Ser 85	Gln	Lys	Asn	Asn	Asn 90	Ğlű	Leu	Pro	Lys	Gln 95	Ãla	
gcg g	gaa	aac	acq		aac	cta	aat	CCG		atc	aac	atc	caa		aac	336
209 5			~~3	9		9		9	2-3	$\alpha \cup \cup$	990	تاب	~ <b>9</b> 9	gge	aay	226

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Ser	Arq	Gly	Gln	Ser	Ala	Ala	Met	Ala 25	Pro	Phe	Gly	Gly	Leu 30	Lys	Ser	
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Gly Lys Lys Lys Phe Glu Thr Leu Ser Tyr Leu Pro Pro Leu Thr Arg 65 70 75 80

- Asp Ser Arg Val Ser Gln Lys Asn Asn Glu Leu Pro Lys Gln Ala 85 90 95
- Ala Glu Asn Thr Leu Asn Leu Asn Pro Val Ile Gly Ile Arg Gly Lys
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- Asp Leu Leu Thr Ser Ala Arg Met Val Leu Leu Gln Ala Val Arg Gln 115 120 125
- Pro Leu His Ser Ala Arg His Val Ala His Phe Ser Leu Glu Leu Lys 130 135 140
- Asn Val Leu Leu Gly Gln Ser Glu Leu Arg Pro Gly Asp Asp Asp Arg 145 150 155 160
- Arg Phe Ser Asp Pro Ala Trp Ser Gln Asn Pro Leu Tyr Lys Arg Tyr 165 170 175
- Met Gln Thr Tyr Leu Ala Trp Arg Lys Glu Leu His Ser Trp Ile Ser 180 185 190
- His Ser Asp Leu Ser Pro Gln Asp Ile Ser Arg Gly Gln Phe Val Ile 195 200 205
- Asn Leu Leu Thr Glu Ala Met Ser Pro Thr Asn Ser Leu Ser Asn Pro 210 215 220
- Ala Ala Wel Lys Arg Phe Phe Glu Thr Gly Gly Lys Ser Leu Leu Asp 225 230 235 240
- Gly Leu Gly His Leu Ala Lys Asp Leu Val Asn Asn Gly Gly Met Pro 245 250 255
- Ser Gln Val Asp Met Asp Ala Phe Glu Val Gly Lys Asn Leu Ala Thr 260 265 270
- Thr Glu Gly Ala Val Val Phe Arg Asn Asp Val Leu Glu Leu Ile Gln 275 280 285
- Tyr Arg Pro Ile Thr Glu Ser Val His Glu Arg Pro Leu Leu Val Val 290 295 300

Pro Pro Gln Ile Asn Lys Phe Tyr Val Phe Asp Leu Ser Pro Asp Lys 315 310 Ser Leu Ala Arg Phe Cys Leu Arg Asn Gly Val Gln Thr Phe Ile Val 330 Ser Trp Arg Asn Pro Thr Lys Ser Gln Arg Glu Trp Gly Leu Thr Thr 340 345 Tyr Ile Glu Ala Leu Lys Glu Ala Ile Glu Val Val Leu Ser Ile Thr Gly Ser Lys Asp Leu Asn Leu Leu Gly Ala Cys Ser Gly Gly Ile Thr Thr Ala Thr Leu Val Gly His Tyr Val Ala Ser Gly Glu Lys Lys Val 390 Asn Ala Phe Thr Gln Leu Val Ser Val Leu Asp Phe Glu Leu Asn Thr Gln Val Ala Leu Phe Ala Asp Glu Lys Thr Leu Glu Ala Ala Lys Arg 420 Arg Ser Tyr Gln Ser Gly Val Leu Glu Gly Lys Asp Met Ala Lys Val 435 Phe Ala Trp Met Arg Pro Asn Asp Leu Ile Trp Asn Tyr Trp Val Asn 455 Asn Tyr Leu Leu Gly Asn Gln Pro Pro Ala Phe Asp Ile Leu Tyr Trp 470 475 Asn Asn Asp Thr Thr Arg Leu Pro Ala Ala Leu His Gly Glu Phe Val Glu Leu Phe Lys Ser Asn Pro Leu Asn Arg Pro Gly Ala Leu Glu Val 500 Ser Gly Thr Pro Ile Asp Leu Lys Gln Val Thr Cys Asp Phe Tyr Cys 520 -515

Val Ala Gly Leu Asn Asp His Ile Thr Pro Trp Glu Ser Cys Tyr Lys

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Ser 545	Ala	Arg	Leu	Leu	Gly 550	Gly	Lys	Cys	Glu	Phe 555	Ile	Leu	Ser	Asn	Ser 560		
Gly	His	Ile	Gln	Ser 565	Ile	Leu	Asn	Pro	Pro 570	Gly	Asn	Pro	Lys	Ala 575	Arg		
Phe	Met	Thr	Asn 580	Pro	Glu	Leu	Pro	Ala 585	Glu	Pro	Lys	Ala	Trp 590	Leu	Glu		
Gln	Ala	Gly 595		His	Ala	Asp	Ser 600	Trp	Trp	Leu	His	Trp 605	Gln	Gln	Trp		
Leu	Ala 610		Arg	Ser	Gly	Lys 615	Thr	Arg	Lys	Ala	Pro 620	Ala	Ser	Leu	Gly		
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cgcatggtcc tgctccaggc ggtgcgccag ccgctgcaca gcgccaggca cgtggcgcat

ttcagcctgg agctgaagaa cgtcctgctc ggccagtcgg agctacgccc aggcgatgac

420

480

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gactcgtggt ggttgcactg gcagcaatgg ctggccgaac gctccggcaa gacccgcaag	1860
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<210> 28

<211> 1137

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<212> DNA

<213> Pseudomonas putida

<220>

<221> CDS

<222> (1)..(1137)

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tct Se:	agg Arg	Gly	caa Gln 20	tcc Ser	gcc Ala	gca Ala	atg Met	gct Ala 25	cca Pro	ttc Phe	ggc Gly	ggc Gly	ctc Leu 30	aaa Lys	tcc Ser	96
ato Mei	g act Thr	gga Gly 35	ttc Phe	cca Pro	gtg Val	aag Lys	aag Lys 40	gtc Val	aac Asn	act Thr	gac Asp	att Ile 45	act Thr	tcc Ser	att Ile	144
aca Thi	a agc Ser 50	aat Asn	ggt Gly	gga Gly	aga Arg	gta Val 55	aag Lys	tgc Cys	atg Met	cag Gln	gtg Val 60	tgg Trp	cct Pro	cca Pro	aťt Ile	192
gg; Gl; 65	a aag / Lys	aag Lys	aag Lys	ttt Phe	gag Glu 70	act Thr	ctt Leu	tcc Ser	tat Tyr	ttg Leu 75	cca Pro	cca Pro	ttg Leu	acc Thr	aga Arg 80	240
ga <sup>t</sup> Asj	tcc Ser	cgg <u>"A</u> rg	gtg Val	agg Arg 85	cca Pro	gaa Glu	atc Ile	gct Ala	gta Val 90	ctt Leu	gat Asp	atc Ile	caa Gln	ggt Gly 95	cag Gln	288
ta Ty:	cgg Arg	gtt Val	tac Tyr 100	acg Thr	gag Glu	ttc Phe	tat Tyr	cgc Arg 105	gcg Ala	gat Asp	gcg Ala	gcc Ala	gaa Glu 110	aac Asn	acg Thr	336
ate Ile	c atc e Ile	ctg Leu 115	Ile	aac Asn	ggc Gly	tcg Ser	ctg Leu 120	gcc Ala	acc Thr	acg Thr	gcc Ala	tcg Ser 125	ttc Phe	gcc Ala	cag Gln	384
ac Th	g gta r Val 130	Arg	aac Asn	ctg Leu	cac His	cca Pro 135	cag Gln	ttc Phe	aac Asn	gtg Val	gtt Val 140	ctg Leu	ttc Phe	gac Asp	cag Gln	432
cc Pr 14	g tat o Tyr 5	tca Ser	ggc	aag Lys	tcc Ser 150	aag Lys	ccg Pro	cac His	aac Asn	cgt Arg 155	cag Gln	gaa Glu	cgg Arg	ctg Leu	atc Ile 160	480
ag Se	c aag r Lys	gag Glu	acc Thr	gag Glu	gcg Ala	cat His	atc Ile	ctc Leu	ctt Leu	gag Glu	ctg Leu	atc Ile	gag Glu	cac His	ttc Phe	528

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				165					170					175		
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tcg Ser	ttc Phe 210	tcg Ser	cca Pro	gtg Val	atc Ile	aac Asn 215	gag Glu	ccg Pro	atg Met	cgc Arg	gac Asp 220	tat Tyr	ctg Leu	gac Asp	cgt Arg	672
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aac Asn	tac Tyr	cgc Arg	cat His 260	gtg Val	agc Ser	agc Ser	ctg Leu	gac Asp 265	agc Ser	cac His	gag Glu	tac Tyr	gca Ala 270	cag Gln	atg Met .	816
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Val	Gly	Arg	Ser	Gln 325	Phe	Ser	Val	Ile	330	( Asp	Ala	ı GIY	Hls	335		1008
gac Asp	atg Met	gag Glu	aac Asn 340	Lys	acc Thr	gcc	tgc Cys	gag Glu 345	Asn	acc Thr	cgc Arg	aat g Asn	gto Val 350	. Met	ctg : Leu	1056
Gl3	ttc Phe	cto Lev 355	ı Lys	r cca	acc Thr	gtg Val	cgt Arg 360	g Glu	cco Pro	c cgc o Arg	caa g Glr	a cgt n Arc 365	ı Tyr	caa Glr	e ccc	1104
gto Val	g cag L Glr 370	ı Glı	r GJ7 A aad	g caq g Gli	g cat n His	gca Ala 375	ı Phe	gco Ala	ato a Ile	c tga e	a					1137

<211> 378

<212> PRT

<213> Pseudomonas putida

<400> 29

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Thr Ser Asn Gly Gly Arg Val Lys Cys Met Gln Val Trp Pro Pro Ile 55

Gly Lys Lys Lys Phe Glu Thr Leu Ser Tyr Leu Pro Pro Leu Thr Arg 75

Asp Ser Arg Val Arg Pro Glu Ile Ala Val Leu Asp Ile Gln Gly Gln 90

Tyr Arg Val Tyr Thr Glu Phe Tyr Arg Ala Asp Ala Ala Glu Asn Thr

Ile Ile Leu Ile Asn Gly Ser Leu Ala Thr Thr Ala Ser Phe Ala Gln 120

Thr Val Arg Asn Leu His Pro Gln Phe Asn Val Val Leu Phe Asp Gln 135 130

Pro Tyr Ser Gly Lys Ser Lys Pro His Asn Arg Gln Glu Arg Leu Ile 150 155 145

Ser Lys Glu Thr Glu Ala His Ile Leu Leu Glu Leu Ile Glu His Phe 170 165

Gln Ala Asp His Val Met Ser Phe Ser Trp Gly Gly Ala Ser Thr Leu 185 180

Leu Ala Leu Ala His Gln Pro Arg Tyr Val Lys Lys Ala Val Val Ser 195 200 205

Ser Phe Ser Pro Val Ile Asn Glu Pro Met Arg Asp Tyr Leu Asp Arg 210 215 220

Gly Cys Gln Tyr Leu Ala Ala Cys Asp Arg Tyr Gln Val Gly Asn Leu 225 230 235 240

Val Asn Asp Thr Ile Gly Lys His Leu Pro Ser Leu Phe Lys Arg Phe 245 250 255

Asn Tyr Arg His Val Ser Ser Leu Asp Ser His Glu Tyr Ala Gln Met 260 265 270

His Phe His Ile Asn Gln Val Leu Glu His Asp Leu Glu Arg Ala Leu 275 280 285

Gln Gly Ala Arg Asn Ile Asn Ile Pro Val Leu Phe Ile Asn Gly Glu 290 295 300

Arg Asp Glu Tyr Thr Thr Val Glu Asp Ala Arg Gln Phe Ser Lys His 305 310 315 320

Val Gly Arg Ser Gln Phe Ser Val Ile Arg Asp Ala Gly His Phe Leu 325 330 335

Asp Met Clu Asn Lys Thr Ala Cys Glu Asn Thr Arg Asn Val Met Leu 340 345 350

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<210> 30

<211> 1149

<212> DNA

<213> Pseudomonas putida

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caggtgtggc	ctccaattgg	aaagaagaag	tttgagactc	tttcctattt	gccaccattg	240
accagagatt	cccgggtgag	gccagaaatc	gctgtacttg	atatccaagg	tcagtatcgg	300
gtttacacgg	agttctatcg	cgcggatgcg	gccgaaaaca	cgatcatcct	gatcaacggc	360
tcgctggcca	ccacggcctc	gttcgcccag	acggtacgta	acctgcaccc	acagttcaac	420
gtggttctgt	tcgaccagcc	gtattcaggc	aagtccaagc	cgcacaaccg	tcaggaacgg	480
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aagcatgtgg	gcagaagcca	gttcagcgtg	atccgcgatg	cgggccactt	cctggacatg	1020
gaga <del>acaaga</del> .	ccgcctgcga	gaacacccgc	aatgtcatgc	tgggcttcct	caagccaacc	1080
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<sup>&</sup>lt;210> 31

<sup>&</sup>lt;211> 519

<sup>&</sup>lt;212> DNA

<sup>&</sup>lt;213> Aeromonas caviae

WO 2004/006657 PCT/AU2003/000903

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<221> CDS

<222> (1)..(519)

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cgg Arg	ttc Phe	ggg Gly	gcg Ala 20	gcg Ala	gag Glu	gta Val	gcc Ala	gcc Ala 25	ttc Phe	gcc Ala	gcg Ala	ctc Leu	tcg Ser 30	gag Glu	gac Asp	96
ttc Phe	aac Asn	ccc Pro 35	ctg Leu	cac His	ctg Leu	gac Asp	ccg Pro 40	gcc Ala	ttc Phe	gcc Ala	gcc Ala	acc Thr 45	acg Thr	gcg Ala	ttc Phe	144
gag Glu	cgg Arg 50	ccc Pro	ata Ile	gtc Val	cac His	ggc Gly 55	atg Met	ctg Leu	ctc Leu	gcc Ala	agc Ser 60	ctc Leu	ttc Phe	tcc Ser	GJÀ āāā	192
ctg Leu 65	ctg Leu	ggc Gly	cag Gln	cag Gln	ttg Leu 70	ccg Pro	ggc Gly	aag Lys	GJÀ āāā	agc Ser 75	atc Ile	tat Tyr	ctg Leu	ggt Gly	caa Gln 80	240
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gag Glu	gtg Val	gag Glu	gtg Val 100	Thr	gcc Ala	ctt Leu	cgc Arg	gag Glu 105	gac · Asp	aag Lys	ccc	atc Ile	gcc Ala 110	acc Thr	ctg Leu	336
acc Thr	acc	cgc Arg	Ile	ttc Phe	acc Thr	caa Gln	ggc Gly 120	Gly	gcc Ala	ctc Leu	gcc Ala	gtg Val 125	acg Thr	G1A aaa	gaa Glu	384
gcc Ala	gtg Val 130	Val	aag Lys	ctg Leu	cct Pro	tca Ser 135	aaa Lys	gct Ala	ttg Leu	ggc	aaa Lys 140	Gly	gtt Val	acc Thr	gag Glu	432
gaa Glu 145	Gln	ttc Phe	aaa Lys	gag Glu	acc Thr 150	Trp	acg Thr	agg Arg	ccg Pro	gga Gly 155	Ala	gct Ala	gga Gly	atg Met	ggc Gly 160	480
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<210> 32

<211> 172

<212> PRT

<213> Aeromonas caviae

<400> 32

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Phe Asn Pro Leu His Leu Asp Pro Ala Phe Ala Ala Thr Thr Ala Phe 35 40 45

Glu Arg Pro Ile Val His Gly Met Leu Leu Ala Ser Leu Phe Ser Gly 50 55 60

Leu Leu Gly Gln Gln Leu Pro Gly Lys Gly Ser Ile Tyr Leu Gly Gin 65 70 75 80

Ser Leu Ser Phe Lys Leu Pro Val Phe Val Gly Asp Glu Val Thr Ala 85 90 95

Glu Val Glu Val Thr Ala Leu Arg Glu Asp Lys Pro Ile Ala Thr Leu 100 105 110

Thr Thr Arg Ile Phe Thr Gln Gly Gly Ala Leu Ala Val Thr Gly Glu
125
120
125

Ala Val Val Lys Leu Pro Ser Lys Ala Leu Gly Lys Gly Val Thr Glu 130 135 140

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Glu Gly Thr Ser Leu Val Val Ala Lys Ser Arg Met 165 170

<210> 33

<211> 598

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<212>	DNA	

## <213> Aeromonas caviae

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<210> 34

<211> 31

<212> DNA

<213> artificial sequence

<220>

<221> misc\_feature

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<400> 34 nnnnnnggat ccatggcttc tatgatatcc t

31

<210> 35

<211> 30

<212> DNA

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خ <b>4213</b>	artificial sequence	
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<210>	46	
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